

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/007,078

DATE: 12/20/2001

TIME: 14:09:27

Input Set : A:\RTS-0236 Sequence Listing.txt

Output Set: N:\CRF3\12202001\J007078.raw

PS

4 <110> APPLICANT: Donna T. Ward
 5 Andrew T. Watt
 7 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF EIF2C1 EXPRESSION
 9 <130> FILE REFERENCE: RTS-0236
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/007,078
 C--> 11 <141> CURRENT FILING DATE: 2001-11-08
 11 <160> NUMBER OF SEQ ID NOS: 88
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 20
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Artificial Sequence
 19 <220> FEATURE:
 21 <223> OTHER INFORMATION: Antisense Oligonucleotide
 23 <400> SEQUENCE: 1
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 28 <211> LENGTH: 20
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Artificial Sequence
 32 <220> FEATURE:
 34 <223> OTHER INFORMATION: Antisense Oligonucleotide
 36 <400> SEQUENCE: 2
 37 atgcattctg cccccaagga 20
 40 <210> SEQ ID NO: 3
 41 <211> LENGTH: 7478
 42 <212> TYPE: DNA
 43 <213> ORGANISM: Homo sapiens
 45 <220> FEATURE:
 47 <220> FEATURE:
 48 <221> NAME/KEY: CDS
 49 <222> LOCATION: (214)...(2787)
 51 <400> SEQUENCE: 3
 52 actggcagct ggccgggagc tcgcagtggg agctgctgca ggctccgcgg cggcgggcaac 60
 53 ggaggctgcg gggggcggcg cgcgagcggc cgggcttggt aggggagccg agcccgggcc 120
 54 gggatcccgga gcagcgagag tgtgggggtac ctaggcccct cacgctggac ttcacagtct 180
 55 ccggggccgcc tgacctccgc acgggtatat ggg atg gaa gcg gga ccc tcg gga 234
 56 Met Glu Ala Gly Pro Ser Gly
 57 1 5
 59 gca gct gcg ggc gct tac ctg ccc ccc ctg cag cag gtg ttc cag gca 282
 60 Ala Ala Ala Gly Ala Tyr Leu Pro Pro Leu Gln Gln Val Phe Gln Ala
 61 10 15 20
 63 cct cgc cgg cct ggc att ggc act gtg ggg aaa cca atc aag ctc ctg 330
 64 Pro Arg Arg Pro Gly Ile Gly Thr Val Gly Lys Pro Ile Lys Leu Leu
 65 25 30 35
 67 gcc aat tac ttt gag gtg gac atc cct aag atc gac gtg tac cac tac 378
 68 Ala Asn Tyr Phe Glu Val Asp Ile Pro Lys Ile Asp Val Tyr His Tyr
 69 40 45 50 55

**Does Not Comply
Corrected Diskette Needed**

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```

71 gag gtg gac atc aag ccg gat aag tgt ccc cgt aga gtc aac cgg gaa      426
72 Glu Val Asp Ile Lys Pro Asp Lys Cys Pro Arg Arg Val Asn Arg Glu
73          60          65          70
75 gtg gtg gaa tac atg gtc cag cat ttc aag cct cag atc ttt ggt gat      474
76 Val Val Glu Tyr Met Val Gln His Phe Lys Pro Gln Ile Phe Gly Asp
77          75          80          85
79 cgc aag cct gtg tat gat gga aag aac att tac act gtc aca gca      522
80 Arg Lys Pro Val Tyr Asp Gly Lys Lys Asn Ile Tyr Thr Val Thr Ala
81          90          95          100
83 ctg ccc att ggc aac gaa cgg gtc gac ttt gag gtg aca atc cct ggg      570
84 Leu Pro Ile Gly Asn Glu Arg Val Asp Phe Glu Val Thr Ile Pro Gly
85          105          110          115
87 gaa ggg aag gat cga atc ttt aag gtc tcc atc aag tgg cta gcc att      618
88 Glu Gly Lys Asp Arg Ile Phe Lys Val Ser Ile Lys Trp Leu Ala Ile
89 120          125          130          135
91 gtg agc tgg cga atg ctg cat gag gcc ctg gtc agc ggc cag atc cct      666
92 Val Ser Trp Arg Met Leu His Glu Ala Leu Val Ser Gly Gln Ile Pro
93          140          145          150
95 gtt ccc ttg gag tct gtg caa gcc ctg gat gtg gcc atg agg cac ctg      714
96 Val Pro Leu Glu Ser Val Gln Ala Leu Asp Val Ala Met Arg His Leu
97          155          160          165
99 gca tcc atg agg tac acc cct gtg ggc cgc tcc ttc ttc tca ccg cct      762
100 Ala Ser Met Arg Tyr Thr Pro Val Gly Arg Ser Phe Phe Ser Pro Pro
101          170          175          180
103 gag ggc tac tac cac ccg ctg ggg ggt ggg cgc gaa gtc tgg ttc ggc      810
104 Glu Gly Tyr Tyr His Pro Leu Gly Gly Gly Arg Glu Val Trp Phe Gly
105          185          190          195
107 ttt cac cag tct gtg cgc cct gcc atg tgg aag atg atg ctc aac att      858
108 Phe His Gln Ser Val Arg Pro Ala Met Trp Lys Met Met Leu Asn Ile
109 200          205          210          215
111 gat gtc tca gcc act gcc ttt tat aag gca cag cca gtg att gag ttc      906
112 Asp Val Ser Ala Thr Ala Phe Tyr Lys Ala Gln Pro Val Ile Glu Phe
113          220          225          230
115 atg tgt gag gtg ctg gac atc agg aac ata gat gag cag ccc aag ccc      954
116 Met Cys Glu Val Leu Asp Ile Arg Asn Ile Asp Glu Gln Pro Lys Pro
117          235          240          245
119 ctc acg gac tct cag cgc gtt cgc ttc acc aag gag atc aag ggc ctg      1002
120 Leu Thr Asp Ser Gln Arg Val Arg Phe Thr Lys Glu Ile Lys Gly Leu
121          250          255          260
123 aag gtg gaa gtc acc cac tgt gga cag atg aag agg aag tac cgc gtg      1050
124 Lys Val Glu Val Thr His Cys Gly Gln Met Lys Arg Lys Tyr Arg Val
125          265          270          275
127 tgt aat gtt acc cgt cgc cct gct agc cat cag aca ttc ccc tta cag      1098
128 Cys Asn Val Thr Arg Arg Pro Ala Ser His Gln Thr Phe Pro Leu Gln
129 280          285          290          295
131 ctg gag agt gga cag act gtg gag tgc aca gtg gca cag tat ttc aag      1146
132 Leu Glu Ser Gly Gln Thr Val Glu Cys Thr Val Ala Gln Tyr Phe Lys
133          300          305          310
135 cag aaa tat aac ctt cag ctc aag tat ccc cat ctg ccc tgc cta caa      1194

```

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136	Gln	Lys	Tyr	Asn	Leu	Gln	Leu	Lys	Tyr	Pro	His	Leu	Pro	Cys	Leu	Gln	
137				315					320					325			
139	gtt	ggc	cag	gaa	caa	aag	cat	acc	tac	ctt	ccc	cta	gag	gtc	tgt	aac	1242
140	Val	Gly	Gln	Glu	Gln	Lys	His	Thr	Tyr	Leu	Pro	Leu	Glu	Val	Cys	Asn	
141			330					335					340				
143	att	gtg	gct	ggg	cag	cgc	tgt	att	aag	aag	ctg	acc	gac	aac	cag	acc	1290
144	Ile	Val	Ala	Gly	Gln	Arg	Cys	Ile	Lys	Lys	Leu	Thr	Asp	Asn	Gln	Thr	
145			345				350					355					
147	tcg	acc	atg	ata	aag	gcc	aca	gct	aga	tcc	gct	cca	gac	aga	cag	gag	1338
148	Ser	Thr	Met	Ile	Lys	Ala	Thr	Ala	Arg	Ser	Ala	Pro	Asp	Arg	Gln	Glu	
149	360				365					370					375		
151	gag	atc	agt	cgc	ctg	atg	aag	aat	gcc	agc	tac	aac	tta	gat	ccc	tac	1386
152	Glu	Ile	Ser	Arg	Leu	Met	Lys	Asn	Ala	Ser	Tyr	Asn	Leu	Asp	Pro	Tyr	
153				380				385					390				
155	atc	cag	gaa	ttt	ggg	atc	aaa	gtg	aag	gat	gac	atg	acg	gag	gtg	aca	1434
156	Ile	Gln	Glu	Phe	Gly	Ile	Lys	Val	Lys	Asp	Asp	Met	Thr	Glu	Val	Thr	
157				395				400					405				
159	ggg	cga	gtg	ctg	ccg	gcg	ccc	atc	ttg	cag	tac	ggc	ggc	cgg	aac	cgg	1482
160	Gly	Arg	Val	Leu	Pro	Ala	Pro	Ile	Leu	Gln	Tyr	Gly	Gly	Arg	Asn	Arg	
161			410				415					420					
163	gcc	att	gcc	aca	ccc	aat	cag	ggt	gtc	tgg	gac	atg	cgg	ggg	aaa	cag	1530
164	Ala	Ile	Ala	Thr	Pro	Asn	Gln	Gly	Val	Trp	Asp	Met	Arg	Gly	Lys	Gln	
165		425				430				435							
167	ttc	tac	aat	ggg	att	gag	atc	aaa	gtc	tgg	gcc	atc	gcc	tgc	ttc	gca	1578
168	Phe	Tyr	Asn	Gly	Ile	Glu	Ile	Lys	Val	Trp	Ala	Ile	Ala	Cys	Phe	Ala	
169	440				445					450				455			
171	ccc	caa	aaa	cag	tgt	cga	gaa	gag	gtg	ctc	aag	aac	ttc	aca	gac	cag	1626
172	Pro	Gln	Lys	Gln	Cys	Arg	Glu	Glu	Val	Leu	Lys	Asn	Phe	Thr	Asp	Gln	
173				460					465				470				
175	ctg	cgg	aag	att	tcc	aag	gat	gcg	ggg	atg	cct	atc	cag	ggt	caa	cct	1674
176	Leu	Arg	Lys	Ile	Ser	Lys	Asp	Ala	Gly	Met	Pro	Ile	Gln	Gly	Gln	Pro	
177			475				480					485					
179	tgt	ttc	tgc	aaa	tat	gca	cag	ggg	gca	gac	agc	gtg	gag	cct	atg	ttc	1722
180	Cys	Phe	Cys	Lys	Tyr	Ala	Gln	Gly	Ala	Asp	Ser	Val	Glu	Pro	Met	Phe	
181			490				495					500					
183	cgg	cat	ctc	aag	aac	acc	tac	tca	ggg	ctg	cag	ctc	att	att	gtc	atc	1770
184	Arg	His	Leu	Lys	Asn	Thr	Tyr	Ser	Gly	Leu	Gln	Leu	Ile	Ile	Val	Ile	
185		505				510						515					
187	ctg	cca	ggg	aag	acg	ccg	gtg	tat	gct	gag	gtg	aaa	cgt	gtc	gga	gat	1818
188	Leu	Pro	Gly	Lys	Thr	Pro	Val	Tyr	Ala	Glu	Val	Lys	Arg	Val	Gly	Asp	
189	520				525					530				535			
191	aca	ctc	ttg	gga	atg	gct	acg	cag	tgt	gtg	cag	gtg	aag	aac	gtg	gtc	1866
192	Thr	Leu	Leu	Gly	Met	Ala	Thr	Gln	Cys	Val	Gln	Val	Lys	Asn	Val	Val	
193				540						545				550			
195	aag	acc	tca	cct	cag	act	ctg	tcc	aac	ctc	tgc	ctc	aag	atc	aat	gtc	1914
196	Lys	Thr	Ser	Pro	Gln	Thr	Leu	Ser	Asn	Leu	Cys	Leu	Lys	Ile	Asn	Val	
197			555					560					565				
199	aaa	ctt	ggt	ggc	att	aac	aac	atc	cta	gtc	cca	cac	cag	cgc	tct	gcc	1962
200	Lys	Leu	Gly	Gly	Ile	Asn	Asn	Ile	Leu	Val	Pro	His	Gln	Arg	Ser	Ala	

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201	570	575	580	
203	gtt ttt caa cag cca gtg ata ttc ctg gga gca gat gtt aca cac ccc	2010		
204	Val Phe Gln Gln Pro Val Ile Phe Leu Gly Ala Asp Val Thr His Pro			
205	585	590	595	
207	cca gca ggg gat ggg aaa aaa cct tct atc aca gca gtg gta ggc agt	2058		
208	Pro Ala Gly Asp Gly Lys Lys Pro Ser Ile Thr Ala Val Val Gly Ser			
209	600	605	610	615
211	atg gat gcc cac ccc agc cga tac tgt gct act gtg cgg gta cag cga	2106		
212	Met Asp Ala His Pro Ser Arg Tyr Cys Ala Thr Val Arg Val Gln Arg			
213	620	625	630	
215	cca cgg caa gag atc att gaa gac ttg tcc tac atg gtg cgt gag ctc	2154		
216	Pro Arg Gln Glu Ile Ile Glu Asp Leu Ser Tyr Met Val Arg Glu Leu			
217	635	640	645	
219	ctc atc caa ttc tac aag tcc acc cgt ttc aag cct acc cgc atc atc	2202		
220	Leu Ile Gln Phe Tyr Lys Ser Thr Arg Phe Lys Pro Thr Arg Ile Ile			
221	650	655	660	
223	ttc tac cga gat ggg gtg cct gaa ggc cag cta ccc cag ata ctc cat	2250		
224	Phe Tyr Arg Asp Gly Val Pro Glu Gly Gln Leu Pro Gln Ile Leu His			
225	665	670	675	
227	tat gag cta ctg gcc att cgt gat gcc tgc atc aaa ctg gaa aag gac	2298		
228	Tyr Glu Leu Leu Ala Ile Arg Asp Ala Cys Ile Lys Leu Glu Lys Asp			
229	680	685	690	695
231	tac cag cct ggg atc act tat att gtg gtg cag aaa cgc cat cac acc	2346		
232	Tyr Gln Pro Gly Ile Thr Tyr Ile Val Val Gln Lys Arg His His Thr			
233	700	705	710	
235	cgc ctt ttc tgt gct gac aag aat gag cga att ggg aag agt ggt aac	2394		
236	Arg Leu Phe Cys Ala Asp Lys Asn Glu Arg Ile Gly Lys Ser Gly Asn			
237	715	720	725	
239	atc cca gct ggg acc aca gtg gac acc aac atc acc cac cca ttt gag	2442		
240	Ile Pro Ala Gly Thr Thr Val Asp Thr Asn Ile Thr His Pro Phe Glu			
241	730	735	740	
243	ttt gac ttc tat ctg tgc agc cac gca ggc atc cag ggc acc agc cga	2490		
244	Phe Asp Phe Tyr Leu Cys Ser His Ala Gly Ile Gln Gly Thr Ser Arg			
245	745	750	755	
247	cca tcc cat tac tat gtt ctt tgg gat gac aac cgt ttc aca gca gat	2538		
248	Pro Ser His Tyr Tyr Val Leu Trp Asp Asp Asn Arg Phe Thr Ala Asp			
249	760	765	770	775
251	gag ctc cag atc ctg acg tac cag ctg tgc cac act tac gta cga tgc	2586		
252	Glu Leu Gln Ile Leu Thr Tyr Gln Leu Cys His Thr Tyr Val Arg Cys			
253	780	785	790	
255	aca cgc tct gtc tct atc cca gca cct gcc tac tat gcc cgc ctg gtg	2634		
256	Thr Arg Ser Val Ser Ile Pro Ala Pro Ala Tyr Tyr Ala Arg Leu Val			
257	795	800	805	
259	gct ttc cgg gca cga tac cac ctg gtg gac aag gag cat gac agt gga	2682		
260	Ala Phe Arg Ala Arg Tyr His Leu Val Asp Lys Glu His Asp Ser Gly			
261	810	815	820	
263	gag ggg agc cac ata tcg ggg cag agc aat ggg cgg gac ccc cag gcc	2730		
264	Glu Gly Ser His Ile Ser Gly Gln Ser Asn Gly Arg Asp Pro Gln Ala			
265	825	830	835	

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```

267 ctg gcc aaa gcc gtg cag gtt cac cag gat act ctg cgc acc atg tac 2778
268 Leu Ala Lys Ala Val Gln Val His Gln Asp Thr Leu Arg Thr Met Tyr
269 840 845 850 855
271 ttc gct tga aggcagaacg ctgttacctc actggataga agaaagcttt ccaagcccca 2837
272 Phe Ala
275 ggagctgtgc cacccaaadc cagaggaagc aaggaggagg gaggtggggg agggaggagt 2897
276 gtaggatgcc ttgtttcctt ctatagaggt ggtgtaagag tggggaacag ggccagcaag 2957
277 acagaccacc agccagaaat ctctgatata aacctcatgt ccccccaccc tcaccccatc 3017
278 ttgtcacatc tggccctgac cccactggac caaaaggggc agcactggtg cccaccatac 3077
279 acacaggtgt ctcattgtgac tcacagtgtc aaagactcat gcttgacagc ttggtaaggt 3137
280 caactctgta gccctgcaga caaaagctgg tttaggtttgg gtttgatact tttagatggga 3197
281 aagtggaggg cttgagaaaag tgggtggggg gaggggaagga ttttttagga gccttaataca 3257
282 gaaaaggact agattttgttt aagaagaaaa atgaaaccag acccagatca atatttttagg 3317
283 atactagatg ttttaattggg ttcagaatcc agttttgtagg aagatttttt aatgggttttg 3377
284 gttgtctctc cccagctgc cccccccac cttaccctta ttcctctctg tccacatttt 3437
285 ctgccccacc ttacttctcc tccctgacag acatccagcc cctagtaata ctttaaggcac 3497
286 tatggcactt agctttgaag tgacacgacc ctgtcttctc tccgcccgtc ggtgggtaac 3557
287 cagtgccttc cctgtaacgg taatgctgca gaactgcaac cttttgtacc tttctttggg 3617
288 gaatgggggtg ggggtgggag agggaggtaga tggggaagaa ataccccaga cccaacaaac 3677
289 ctccagccag aaagccagct attttgcaat tgaagggaatt gacttctca ttcattgagc 3737
290 tttttaaaag atcacaacct caagatggtt aaaatccatt gacatttgca ctttcaaaca 3797
291 tgacaagtct cggagctgct gagatgacag gccctggcc tttccactta tgccctcttt 3857
292 tctccttatt cctcctacct ccgccccgc ccaggtctgg agttactttc atagcatttt 3917
293 tcaactcttg cttcttttct cccttgatgg tcaagtctct tatgtttcaa tatttcttaa 3977
294 ctgggggtgc ttataacaaa aaactcttag gtctaaaatg agaaaaaaga gagaaaacaa 4037
295 aatgttattt ttataccata acttgagtgt attgccaaaa tttggaaatc cttcccatgc 4097
296 ctgatgagtt tatatccag aaacattgag ccatacagaat gaactgtgta cctgatttgt 4157
297 tctctgacct ggctaggtag ggaggggggt gttatcgccc caagatgggg tccaggtccc 4217
298 atccttctct tgtgcagata ataccttttt cttgctatag cctccctcct ctgcaactgtc 4277
299 ctgcaactct tcttgcaagt gcatcttttt ccttcccctg gactgtctc tgaccctttg 4337
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305 cttcagtgtg gaatttctc tttgaggagc ctgggcttgg atctatcctg atctggtgat 4697
306 gaagccatga ttactttaga cctagcccag gcttggaggc cagctggagg aagaagggtc 4757
307 taaatcctgg cctgtagagt tagaactacc atttcctccc cttagctgcc cttgtatgac 4817
308 ccgattttgc tatgcaaaac aatctatccc aggttctgtt ctggttggct acattgttca 4877
309 gcaactcaca aaacgtagca caaacattca ttatggagaa agcatcagga ctgttgagta 4937
310 actcctcctt tacttttttc ctgctggcta cagcatgggg tgccctatag gcacaagccc 4997
311 agctgaagaa cagaatggag ggctctggga ggaggcagct cactggagag cctacattcc 5057
312 ttacacaagt gcctaaagag agtgatgcta aactccatc tgccctgtcc attgccttca 5117
313 tatacagtct acttctgtt ctgtcaccct ttggggaggg gacttctcct gggacagtgg 5177
314 gctctgcagt ttctccactt ggatacattt tggggctagg atcagggcac tattcctgga 5237
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316 ccagcaaca agtttgtgtt ctctcctttt ctctctttgc ctcactctct ccagttgggt 5357
317 ttcagctggg gcttgaaatg cttttttagc cttttgacgt ggcttatgcc attcaagaaa 5417
318 taaaagcaa gagaatcagc tttgggcaat gacaagaaat gagttcttac tctgattttt 5477

```

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.



VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:825 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:826 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:939 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:940 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:973 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:974 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:975 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:2246 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:2249 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:88
L:2249 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:2253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:88
L:2253 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
L:2254 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:88
L:2254 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4